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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=5; day=29; hr=17; min=14; sec=58; ms=546;]

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Reviewer Comments:

<110> ALBERT EINSTEIN COLLEGE OF MEDICINE OF YESHIVA UNIVERSITY
MELNICK, Ari M.
LICHT, Jonathan D.
PRIVÉ, Gilbert G.
AHMAD, Khaja Farid

Please remove the foreign accent mark from the fourth applicant's name:
foreign accent marks are non-ASCII characters, and cannot be processed.

<210> 10
<211> 17
<212> PRT
<213> Artificial

<220>
<223> consensus sequence

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> amino acid residue is Leu, Gly, or Tyr

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<223> amino acid residue is Val, Ile, or Arg

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<222> (3)..(3)
<223> amino acid residue is Ala, Thr, or Ser

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<400> 10

Leu Val Ala Thr Val Lys Glu Ala Gly Arg Ser Ile His Glu Ile Pro
1 5 10 15

Arg

The above <220>-<223> sections stating that the amino acids at those locations can also represent another amino acid are incorrect (e.g., for location 1, amino acid residue is Leu, Gly, or Tyr). "Leu" at location 1 can only represent itself. Please use "Xaa's" instead, and explain which amino acid residues they can represent.

Application No: 10582662

Version No: 1.0

Input Set:

Output Set:

Started: 2008-05-28 14:21:46.010

Finished: 2008-05-28 14:21:47.829

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 819 ms

Total Warnings: 20

Total Errors: 0

No. of SeqIDs Defined: 34

Actual SeqID Count: 34

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W 213	Artificial or Unknown found in <213> in SEQ ID (19)
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W 213	Artificial or Unknown found in <213> in SEQ ID (29)
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Input Set:

Output Set:

Started: 2008-05-28 14:21:46.010
Finished: 2008-05-28 14:21:47.829
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 819 ms
Total Warnings: 20
Total Errors: 0
No. of SeqIDs Defined: 34
Actual SeqID Count: 34

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

<210> 1
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<213> Homo sapiens

<400> 1

Leu Val Ala Thr Val Lys Glu Ala Gly Arg Ser Ile His Glu Ile Pro
1 5 10 15

Arg

<210> 2
<211> 17
<212> PRT
<213> Homo sapiens

<400> 2

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1 5 10 15

Arg

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<212> PRT
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Gly

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<211> 21
<212> PRT
<213> Homo sapiens

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Pro Arg Glu Glu Leu

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Pro Arg Gln Asp Ile
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Pro Gly Pro Ser Pro
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Pro Arg Glu Glu Leu Arg His Thr Pro Glu Leu Pro Leu
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<400> 9

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1 5 10 15

Pro Gly Pro Ser Pro Asn Glu Glu Asn Asn Gly Lys
20 25

<210> 10
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<212> PRT
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<223> consensus sequence

<220>
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<222> (1)..(1)
<223> amino acid residue is Leu, Gly, or Tyr

<220>
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<222> (2)..(2)
<223> amino acid residue is Val, Ile, or Arg

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<222> (4)..(4)
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<222> (6)..(6)
<223> amino acid residue is Lys or Ile

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<400> 10

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Leu Val Ala Thr Val Lys Glu Ala Gly Arg Ser Ile His Glu Ile Pro
1           5           10          15

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Arg

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<211> 129
<212> PRT
<213> Homo sapiens

<400> 11

Met Ala Ser Pro Ala Asp Ser Cys Ile Gln Phe Thr Arg His Ala Ser
1 5 10 15

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20 25 30

Asp Val Val Ile Val Val Ser Arg Glu Gln Phe Arg Ala His Lys Thr
35 40 45

Val Leu Met Ala Cys Ser Gly Leu Phe Tyr Ser Ile Phe Thr Asp Gln
50 55 60

Leu Lys Cys Asn Leu Ser Val Ile Asn Leu Asp Pro Glu Ile Asn Pro
65 70 75 80

Glu Gly Phe Cys Ile Leu Leu Asp Phe Met Tyr Thr Ser Arg Leu Asn
85 90 95

Leu Arg Glu Gly Asn Ile Met Ala Val Met Ala Thr Ala Met Tyr Leu
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Gln Met Glu His Val Val Asp Thr Cys Arg Lys Phe Ile Lys Ala Ser
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Glu

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20 25 30

Val Ile Val Val Ser Arg Glu Gln Phe Arg Ala His Lys Thr Val Leu
35 40 45

Met Ala Cys Ser Gly Leu Phe Tyr Ser Ile Phe Thr Asp Gln Leu Lys
50 55 60

Arg Asn Leu Ser Val Ile Asn Leu Asp Pro Glu Ile Asn Pro Glu Gly
65 70 75 80

Phe Asn Ile Leu Leu Asp Phe Met Tyr Thr Ser Arg Leu Asn Leu Arg
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Glu Gly Asn Ile Met Ala Val Met Ala Thr Ala Met Tyr Leu Gln Met
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Glu His Val Val Asp Thr Cys Arg Lys Phe Ile Lys Ala Ser Glu
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 <400> 18
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 <210> 19
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Val Val Pro Gly Pro Ser Pro Asn Glu
20 25

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<212> PRT
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Pro

<210> 33
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Pro

<210> 34
<211> 17
<212> PRT
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<400> 34

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1 5 10 15

Pro